Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates
GEN mouse **Cr2** gene Muridae : disease susceptibility gene

L29 ANSWER 2 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN **2001:313481** BIOSIS
DN **PREV200100313481**
TI **Structure** of **complement receptor 2** in complex with its C3d ligand.
AU Szakonyi, Gerda; Guthridge, Joel M.; Li, Lawei; Young, Kendra; **Holers, V. Michael**; **Chen, Xiaojiang S. (1)**
CS (1) Department of Biochemistry and Molecular Genetics, School of Medicine, University of Colorado Health Science Center, Denver, CO, 80262: Xiaojiang.Chen@uchsc.edu USA
SO Science (Washington D C), (1 June, 2001) Vol. 292, No. 5522, pp. 1725-1728. print.
ISSN: 0036-8075.
DT Article
LA English
SL English
AB **Complement receptor 2** (**CR2**/CD21) is an important receptor that amplifies B lymphocyte activation by bridging the innate and adaptive immune systems. **CR2** ligands include complement C3d and Epstein-Barr virus glycoprotein 350/220. We describe the **x-ray structure** of this **CR2** domain in complex with C3d at 2.0 angstroms. The **structure** reveals extensive main chain interactions between C3d and only one short consensus repeat (SCR) of **CR2** and substantial SCR side-side packing. These results provide a detailed understanding of receptor-ligand interactions in this protein family and reveal potential target sites for molecular drug design.
CC Cytology and Cytochemistry - Animal *02506
Biochemical Studies - General *10060
Blood, Blood-Forming Organs and Body Fluids - Blood and Lymph Studies *15002
Blood, Blood-Forming Organs and Body Fluids - Blood Cell Studies *15004
Immunology and Immunochemistry - General; Methods *34502
IT Major Concepts
Biochemistry and Molecular Biophysics
IT Parts, Structures, & Systems of Organisms
B lymphocyte: blood and lymphatics, immune system; immune system: immune system
IT Chemicals & Biochemicals
C3d ligand; **complement receptor 2** [CD21, **CR2**]; short consensus repeat [SCR]
IT Miscellaneous Descriptors
receptor-ligand interactions; **x-ray structure**

L29 ANSWER 3 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN **2000:389341** BIOSIS
DN **PREV200000389341**
TI **CR2**/CD21 SCR1,2 domain ligand binding, physical properties and **structural** analysis.
AU Guthridge, J. (1); Rakstang, J.; Young, K.; Hinshelwood, J.; Garrias, M. R.; Moore, W.; Perkins, S. J.; Overduin, M.; Lambris, J. D.; Karp, D.; Hannan, J.; **Holers, V. M.**
CS (1) Univ. of Colorado Hlth Sci Ctr, Denver, CO USA
SO Immunopharmacology, (August, 2000) Vol. 49, No. 1-2, pp. 49. print.
Meeting Info.: XVIIIth International Complement Workshop Salt Lake City, Utah, USA July 23-27, 2000
ISSN: 0162-3109.
DT Conference

LA English
SL English
CC Immunology and Immunochemistry - General; Methods *34502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Cytology and Cytochemistry - Animal *02506
Cytology and Cytochemistry - Human *02508
Blood, Blood-Forming Organs and Body Fluids - Blood and Lymph Studies *15002
Blood, Blood-Forming Organs and Body Fluids - Blood Cell Studies *15004
BC Hominidae 86.15
IT Major Concepts
Immune System (Chemical **Coordination** and Homeostasis); Methods and Techniques
IT Parts, Structures, & Systems of Organisms
B lymphocytes: blood and lymphatics, immune system
IT Chemicals & Biochemicals
CD21; SCR1,2; **complement receptor 2** [**CR2**]
IT Methods & Equipment
NMR: analytical method
IT Miscellaneous Descriptors
Meeting Abstract; Meeting Poster
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L19 ANSWER 4 OF 5 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN **1998:521721** BIOSIS
DN **PREV199800521721**
TI **Structural** analysis of recombinant human CD21 ligand binding domains.
AU Guthridge, J. M. (1); Aslam, M.; Perkins, S. J.; **Holers, V. M. (1)**
CS (1) Div. Rheumatol., Univ. Colorado Health Sci. Cent., Denver, CO USA
SO Molecular Immunology, (April-May, 1998) Vol. 35, No. 6-7, pp. 354.
Meeting Info.: XVII International Complement Workshop Rhodes, Greece October 11-16, 1998
ISSN: 0161-5890.
DT Conference
LA English
CC Immunology and Immunochemistry - General; Methods *34502
Cytology and Cytochemistry - General *02502
Biochemical Studies - General *10060
Blood, Blood-Forming Organs and Body Fluids - General; Methods *15001
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
IT Major Concepts
Biochemistry and Molecular Biophysics; Immune System (Chemical **Coordination** and Homeostasis)
IT Chemicals & Biochemicals
complement receptor type 2 (CD21): B lymphocyte cell surface molecule, human, ligand binding domain, recombinant, **structural** analysis; factor H: SCR family protein
IT Miscellaneous Descriptors
immune response; Meeting Abstract
RN 206968-01-6 (FACTOR H)

L19 ANSWER 5 OF 5 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN **1995:294062** BIOSIS

AN PREV199598308362
TI Characterization of a **complement receptor 2** (**CR2**, CD21) ligand binding site for C3: An initial **model** of ligand interaction with two linked short consensus repeat modules.
AU Molina, Hector; Perkins, Stephen J.; Sutcliffe, Joel; Sorka, John; Kinoshita, Taroh; **Holers, V. Michael (1)**
CS (1) Univ. Colorado Health Sci. Cent., Box B-115, 4200 E. Ninth Ave., Denver, CO 80262 USA
SO Journal of Immunology, (1995) Vol. 154, No. 12, pp. 6416-6423. ISSN: 0022-1767.
DT Article
LA English.
AB Human **CR2** (CD21, EBV receptor) is an approximately 145-kDa receptor and a member of the regulators of complement activation gene family. Regulators of complement activation proteins are characterized by the presence of repeating motifs of 60 to 70 amino acids that are designated short consensus repeats (SCR). **CR2** serves as a receptor for four distinct ligands. Three of these ligands (complement C3, gp350 220 of EBV, and CD23) interact with the amino terminal 2 of 15 SCR (SCR 1 and 2). Previous studies have determined that at least four sites are important in allowing **CR2** to efficiently bind EBV. Two of these sites are also important for binding mAb OKB7, a reagent that blocks both EBV and iC3b/C3dg binding to **CR2**. We have identified and characterized important sites of iC3b ligand binding by utilizing human-mouse **CR2** chimeras, a rat anti-mouse **CR2** mAb designated 4E9 that blocks receptor binding to C3, and human **CR2** -derived peptides. In addition to demonstrating an important role for the same sequence in SCR 1 that is part of the mAb OKB7 and EBV binding site, we have identified a new region within SCR 2 that interacts with C3. These results, when compared with a **model** of a dual SCR solution **structure** derived from human factor H SCR, predict that two distinct largely surface-exposed sites on **CR2** interact with iC3b. A relative twist of 130 degree about the long **axis** of the second SCR in this **model** would be necessary for these sites to form a single patch for iC3b binding on **CR2**.
CC Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Methods - Carbohydrates *10058
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biochemical Studies - Carbohydrates 10068
Biophysics - General Biophysical Techniques *10504
Biophysics - Membrane Phenomena *10506
Blood, Blood-Forming Organs and Body Fluids - General; Methods *15001
Blood, Blood-Forming Organs and Body Fluids - Lymphatic Tissue and Reticuloendothelial System *15008
BC Hominidae *86215
IT Major Concepts
Blood and Lymphatics (Transport and Circulation); Membranes (Cell Biology); Methods and Techniques
IT Miscellaneous Descriptors
ANALYTICAL METHOD; MOLECULAR **MODELING**; SPECTROSCOPY; **STRUCTURE**
ORGN Super Taxa
Hominidae; Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L29 ANSWER 6 OF 8 BIOSIS COPYRIGHT 2001 BIOLOGICAL ABSTRACTS INC.
AN **1993:312892** BIOSIS
AN **PREV199345019417**
TI Identification of C3 binding sites within human **complement receptor 2** (**CR2**.

AU Molina, H. D. [...]; Brenner, C.; Kinoshita, T.; **Holers, V. M.**
CS [...] HHMI, Wash. Univ. Sch. Med., St. Louis, MO [illegible] USA
SO Journal of Immunology, 1990 Vol. 144, No. 8 PART 2, pp. 14A.
Meeting Info.: Joint Meeting of the American Association of Immunologists and the Clinical Immunology Society Denver, Colorado, USA May 21-25, 1990
ISSN: 0022-1767.
DT Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals [illegible]
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - Molecular Properties and Macromolecules *10506
Metabolism - Proteins, Peptides and Amino Acids *13012
Immunology and Immunochemistry - Immunopathology, Tissue Immunology *34504
BC Hominidae *86015
IT Major Concepts
Biochemistry and Molecular Biophysics; Clinical Immunology (Human Medicine, Medical Sciences); Metabolism
IT Sequence Data
amino acid sequence; molecular sequence data
IT Miscellaneous Descriptors
ABSTRACT; SHORT CONSENSUS REPEAT; **STRUCTURE**-ACTIVITY RELATIONSHIP
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
Hominidae (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L29 ANSWER 7 OF 9 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN **1992:38031** BIOSIS
DN **BR42:14181**
TI ANALYSIS OF THE ACTIVITIES OF RECOMBINANT MOUSE CR1 **CR2** **CR2** AND B1 THE CRRY GENE PRODUCT A FAMILY OF MOLECULES WITH **STRUCTURAL** AND FUNCTIONAL HOMOLOGIES TO THE HUMAN MEMBRANE RCA GENE FAMILY.
AU **HOLERS V M**; KINOSHITA T; WONG W; BRENNER C; MOLINA H
CS HHMI WASH. UNIV. SCH. MED., ST. LOUIS, MO. 63110, USA.
SO PROCEEDINGS OF THE COMPLEMENT IN DISEASE WORKSHOP, CARDIFF, WALES, UK, SEPTEMBER 21-23, 1991. CLIN EXP IMMUNOL. (1991) 86 (SUPPL 1), 3-4.
CODEN: CEXIAL. ISSN: 0009-9104.
DT Conference
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Animal *09036
Comparative Biochemistry, General *10010
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - Molecular Properties and Macromolecules *10506
Immunology and Immunochemistry - General; Methods *34502
BC Hominidae 86015
Muridae 86375
IT Miscellaneous Descriptors
ABSTRACT

L29 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN **1990:427514** BIOSIS
DN **BA90:88315**
TI **STRUCTURAL** REQUIREMENTS FOR THE B-BLYSTEIN-BARR VIRUS RECEPTOR **CR2**-CD21 LIGAND BINDING INTERNALIZATION AND VIRAL INFECTION.

AU CAREL J-C; MYONES B L; FRACIER S; **HOLERS V M**
CS INST. NATL. SANTE RECH. MED., Nice, 4 B. ST. VINCENT DE PAUL, PARIS, FR.
SO J BIOL CHEM, [illegible]
CODEN: JBCHA3. ISSN: [illegible]
FS BA; OLD
LA English
AB The **structure** of **CR2**, the human C3d,g EBV receptor (**CR2**/CD21), consists of 15 or 16 60-70 amino acid repeats called short consensus repeats (SCRs) followed by a transmembrane and a 34-amino acid intracytoplasmic domain. Functions of **CR2** include binding the human complement component C3d,g when it is covalently attached to targets or cross-linked in the fluid phase. In addition, **CR2** binds the Epstein-Barr virus (EBV) and mediates internalization of EBV and subsequent infection of cells. In order to explore functional roles of the repetitive extracytoplasmic SCR **structure** and the intracytoplasmic domain of **CR2**, we have created truncated **CR2** (rCR2) mutants bearing serial deletions of extracytoplasmic SCRs and also the intracytoplasmic tail. We then stably transfected these rCR2 mutants into two cell lines, murine fibroblast L cells and human erythroleukemic K562 cells. Phenotypic analysis of these expressed mutants revealed that 1) The C3d,g- and EBV-binding sites are found in the two amino-terminal SCRs of **CR2**, 2) expression of SCRs 3 and 4 is further required for high affinity binding to soluble cross-linked C3d,g, 3) the intracytoplasmic domain of **CR2** is not required for binding C3d,g or EBV but is necessary for internalization of cross-linked C3d,g as well as for EBV infection of cells, 4) monoclonal anti-**CR2** antibodies with similar activities react with single widely separated epitopes, and 5) no functional roles can yet be clearly assigned to SCRs 5-15, as rCR2 mutants not containing these SCRs show no major differences from wild-type rCR2 in binding or internalizing cross-linked C3d,g or mediating EBV binding and infection.
CC Cytology and Cytochemistry - Human *02008
Biochemical Methods - Proteins, Peptides and Amino Acids 10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - Molecular Properties and Macromolecules *10506
Biophysics - Membrane Phenomena *10508
Virology - Animal Host Viruses *33506
Medical and Clinical Microbiology - Virology *36006
DC Herpesviridae and/or Herpesviridae 02220
Hominidae 86215
IT Miscellaneous Descriptors
HUMAN COMPLEMENT COMPONENT C-3D

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FILE LAST UPDATED: 7 Nov 2002 (20021107/ED)

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L63 ANSWER 1 OF 14 HCAPLUS COPYRIGHT 2002 ACS
AN 2002:624235 HCAPLUS
DN 137:199933
TI The **crystal structure** of human CD21: Implications for Epstein-Barr virus and C3d binding
AU Prota, Andrea E.; Sage, David R.; Stehle, Thilo; Fingeroth, Joyce D.
CS Beth Israel Deaconess Medical Center, Harvard Institutes of Medicine, Harvard Medical School, Boston, MA, 02115, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2002), 99(16), 10641-10646
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
CC 15-4 (Immunochemistry)
AB Human **complement receptor type 2** (CD21) is the cellular receptor for Epstein-Barr virus (EBV), a human tumor virus. The N-terminal two short consensus repeats (SCR1-SCR2) of the receptor interact with the EBV glycoprotein gp350/220 and also with the natural CD21 ligand C3d. Here the authors present the **crystal** structure of the CD21 SCR1-SCR2 fragment in the absence of ligand and demonstrate that it is able to bind EBV. Based on a functional anal. of wild-type and mutant CD21 and **mol.** modeling, the authors identify a likely region for EBV attachment and demonstrate that this region is not involved in the interaction with C3d. A comparison with the previously detd. structure of CD21 SCR1-SCR2 in complex with C3d shows that, in both cases, CD21 assumes compact V-shaped conformations. However, the anal. reveals a surprising degree of flexibility at the SCR1-SCR2 interface, suggesting interactions between the two domains are not specific. The authors present evidence that the V-shaped conformation is induced by deglycosylation of the protein, and that physiol. glycosylation of CD21 would result in a more extended conformation, perhaps with addnl. epitopes for C3d binding.
ST **crystal** structure CD21 antigen Epstein Barr virus
IT Human herpesvirus 4
(binding site on human CD21 antigen for)
IT Human
(**crystal** structure of human CD21 antigen)
IT **Crystal structure**
Molecular modeling
(of human CD21 antigen)
IT Oligosaccharides, Biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(of human CD21 antigen in relation to conformation)
IT **Complement receptors**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**type 2**; **crystal** structure of)
IT 90295-45-0, Complement C3d
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(binding site on human CD21 antigen for)
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE

(1) Ascherio, A; J Am Med Sci 2001, V321, P305 HCAPLUS
(2) Aubry, J; J Immunol 1994, V152, P5405 HCAPLUS
(3) Barlow, P; J Mol Biol 1994, V237, P628 HCAPLUS
(4) Brunger, A; Science 1987, V235, P458
(5) Carel, J; J Biol Chem 1990, V265, P12293 HCAPLUS
(6) Carson, M; J Mol Graph 1987, V5, P105 HCAPLUS
(7) Casasnovas, J; EMBO J 1994, V13, P1931 HCAPLUS
(8) Chang, B; Infectious Mononucleosis 1st
(9) Clemenza, L; J Immunol 2000, V165, P2878 HCAPLUS
(10) Collaborative Computing Project; Acta Crystallogr D 1994, V50 , P760
(11) Decube, B; Blood, in press 2002
(12) Epstein, M; Lancet 1964, V1, P702
(13) Fingeroth, J; J Immunol 1990, V144, P3458 HCAPLUS
(14) Fingeroth, J; J Virol 1988, V62, P1442 HCAPLUS
(15) Fingeroth, J; J Virol 1999, V73, P2115 HCAPLUS
(16) Fingeroth, J; Proc Natl Acad Sci USA 1984, V81, P4510 HCAPLUS
(17) Fingeroth, J; Proc Natl Acad Sci USA 1989, V86, P2442 HCAPLUS
(18) Frade, R; Proc Natl Acad Sci USA 1985, V82, P1490
(19) Gillam, S; Gene 1979, V8, P81 HCAPLUS
(20) Guthridge, J; Biochemistry 2001, V40, P5931 HCAPLUS
(21) Henderson, C; J Mol Biol 2001, V307, P829 HCAPLUS
(22) IARC Working Group on the Evaluation of Carcinogenic Risks to Humans; IARC Monographs on the Evaluation of Carcinogenic Risks to Humans 1997, V70
(23) James, C; J Clin Invest 1997, V100, P3019 HCAPLUS
(24) Jones, T; Acta Crystallogr A 1991, V47, P110
(25) Lowell, C; J Exp Med 1989, V170, P1931 HCAPLUS
(26) Maisner, A; J Virol 1996, V70, P4973 HCAPLUS
(27) Martin, D; J Exp Med 1991, V174, P1299 HCAPLUS
(28) Martin, W; Mol Cell 2001, V7, P867 HCAPLUS
(29) Molina, H; J Biol Chem 1991, V266, P12173 HCAPLUS
(30) Molina, H; J Immunol 1995, V154, P5426 HCAPLUS
(31) Moore, M; J Virol 1991, V67, P6025
(32) Navaza, J; Acta Crystallogr A 1994, V50, P157
(33) Nemerow, G; J Virol 1985, V55, P347 HCAPLUS
(34) Nemerow, G; J Virol 1987, V61, P1416 HCAPLUS
(35) Nicholls, A; Proteins 1991, V11, P281 HCAPLUS
(36) Otwinowski, Z; Methods Enzymol 1997, V276, P307 HCAPLUS
(37) Prodinger, W; J Immunol 1998, V161, P4604 HCAPLUS
(38) Reid, K; Immunol Today 1989, V10, P177 MEDLINE
(39) Rickinson, A; Field's Virology 2001, P2575
(40) Ross, G; Scand J Immunol 1986, V5, P99 HCAPLUS
(41) Sanchez, L; Science 1999, V283, P1914 HCAPLUS
(42) Seed, B; Proc Natl Acad Sci USA 1987, V84, P3365 HCAPLUS
(43) Slaw, M; J Immunol 1986, V136, P4146
(44) Smith, B; Cell 2002, V108, P769 HCAPLUS
(45) Southern, P; J Mol Appl Genet 1982, V1, P327 HCAPLUS
(46) Steele, T; Innate Immunity, in press 2002
(47) Szakonyi, G; Science 2001, V292, P1739 HCAPLUS
(48) Tanner, J; Cell 1987, V50, P203

L53 ANSWER 2 OF 15 HCAPLUS COPYRIGHT 2002 ACS
AN 2001:832574 HCAPLUS
DN 136:11[illegible]
TI Epitope mapping using the **X-ray crystallographic structure** of **complement receptor type 2** (**CR2**)/CD21: identification of a highly inhibitory monoclonal antibody that directly recognizes the **CR2**-C3d interface
AU Guthridge, Joel M.; Young, Kendra; Hipp, Matthew S.; Carroll, Maria-Rossa; Szakonyi, Gerda; **Chen, Xiaojiang S.**; Mulligan, Angela; Donoghue, Eileen; James, Judith A.; Lambris, John D.; Moir, Susan A.; Perkins, Stephen J.; **Holers, V. Michael**
CS Departments of Medicine and Immunology, University of Colorado Health

Sciences Center, Denver, CO, 80262, USA
SO Journal of Immunology (2001), 167(1), 378-387
CODEN: JOIMA3; ISSN: 0022-1767
PB American Association of Immunologists
DT Journal
LA English
CC 15-4 (Immunochemistry)
AB **Complement receptor type 2**
CR2/CD21 is a B lymphocyte cell membrane 3d [illegible] receptor that plays a central role in the immune response. Human **CR2** is also the receptor for the EBV viral membrane glycoprotein gp350/220. Both C3d and gp350/220 bind **CR2** within the first two of 15-16 repetitive domains that have been designated short consensus/complement repeats. Many mAbs react with human **CR2**; however, only one currently available mAb is known to block both C3d/iC3b and gp350/220 binding. The authors have used a recombinant form of human **CR2** contg. the short consensus/complement repeat 1-2 ligand-binding fragment to immunize **Cr2**-/- mice. Following fusion, the authors identified and further characterized four new anti-**CR2** mAbs that recognize this fragment. Three of these inhibited binding of **CR2** to C3d and gp350/220 in different forms. The authors have detd. the relative inhibitory ability of the four mAbs to block ligand binding, and the authors have used overlapping peptide-based approaches to identify linear epitopes recognized by the inhibitory mAbs. Placement of these epitopes on the recently solved **crystal** structure of the **CR2**-C3d complex reveals that each inhibitory mAb recognizes a site either within or adjacent to the **CR2**-C3d contact site. One new mAb, designated 171, blocks **CR2** receptor-ligand interactions with the greatest efficiency and recognizes a portion of the C3d contact site on **CR2**. Thus, the authors have created an anti-human **CR2** mAb that blocks the C3d ligand by direct contact with its interaction site, and the authors have provided confirmatory evidence that the C3d binding site seen in its **crystal** structure exists in soln.
ST epitope antibody complement receptor **CR2**; CD21 antigen monoclonal antibody epitope; complement C3d binding site **CR2** receptor
IT Immunoglobulins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(G1, monoclonal; epitopes on human complement receptor **CR2** for)
IT **Protein motifs**
(SCR (short consensus repeat); characterization of interaction site for C3d on human complement receptor **CR2**)
IT Human
(characterization of epitopes for monoclonal antibodies and interaction site for C3d on complement receptor **CR2**)
IT Peptides, biological studies
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(epitopes on human complement receptor **CR2** for monoclonal antibodies)
IT Epitopes
(for monoclonal antibodies to human complement receptor **CR2**)
IT Glycoproteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(gp350; binding site on human complement receptor **CR2** for)
IT **Molecular modeling**
(of epitopes on human complement receptor **CR2**)
IT **Complement receptors**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
type 2; characterization of epitopes for monoclonal antibodies and interaction site [illegible]

IT 91245-48-1, Complement 3d
RL: BSU (Biological study, unclassified ; PRPH (Biological study
(binding site in human complement receptor CR2 for
IT 390356-50-3 390356-51-4 390356-52-5
RL: BSU (Biological study, unclassified ; PRP (Properties ; BIOL
(Biological study)
epitopes on human complement receptor CR2 for monoclonal
antibodies)
RE.CNT 82 THERE ARE 82 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Ahearn, J; Adv Immunol 1988, V44, P1 HCAPLUS
(2) Ahearn, J; Immunity 1996, V4, P251 HCAPLUS
(3) Ascherio, A; Epidemiology 2000, V11, P220 MEDLINE
(4) Aubry, J; Nature 1992, V358, P505 HCAPLUS
(5) Brackle, S; Eur J Immunol 1997, V27, P122 HCAPLUS
(6) Bayer, V; J Exp Med 1991, V173, P1151 HCAPLUS
(7) Carel, J; J Biol Chem 1990, V265, P12293 HCAPLUS
(8) Carter, R; Science 1992, V256, P105 HCAPLUS
(9) Cohen, J; N Engl J Med 2001, V343, P481 MEDLINE
(10) Cooper, N; Annu Rev Immunol 1988, V6, P85 HCAPLUS
(11) Croix, A; J Exp Med 1996, V183, P1857
(12) Dempsey, P; Science 1996, V271, P348 HCAPLUS
(13) Pearson, D; Annu Rev Immunol 1995, V13, P127 HCAPLUS
(14) Pearson, D; Semin Immunol 1998, V10, P355 HCAPLUS
(15) Pingerath, J; Proc Natl Acad Sci USA 1984, V81, P4510 HCAPLUS
(16) Geysen, H; J Immunol Methods 1987, V102, P259 HCAPLUS
(17) Grosjean, I; Eur J Immunol 1994, V24, P2982 HCAPLUS
(18) Guthridge, J; Biochemistry 2001, V40, P5931 HCAPLUS
(19) Heath, S; Nature 1995, V377, P680
(20) Hedrick, J; J Immunol 1994, V153, P4418 HCAPLUS
(21) Holers, V; J Immunol 1998, V161, P5041 MEDLINE
(22) Hourcade, D; Adv Immunol 1989, V45, P381 HCAPLUS
(23) Iida, K; J Exp Med 1983, V158, P1021 HCAPLUS
(24) James, J; J Clin Invest 1998, V101, P3018
(25) James, J; J Immunol 1994, V153, P2074 HCAPLUS
(26) James, J; J Immunol 1995, V155, P4018 HCAPLUS
(27) Joling, P; J Immunol 1993, V150, P1065 HCAPLUS
(28) Kacani, L; J Virol 2000, V74, P7997 HCAPLUS
(29) Kalli, K; J Immunol 1991, V147, P590 HCAPLUS
(30) Levy, E; Clin Exp Immunol 1993, V90, P235 HCAPLUS
(31) Liu, Y; Eur J Immunol 1991, V21, P1107 HCAPLUS
(32) Martin, D; J Exp Med 1991, V174, P1299 HCAPLUS
(33) Muir, S; J Exp Med 2000, V192, P637 HCAPLUS
(34) Molina, H; J Biol Chem 1266, P12173 HCAPLUS
(35) Molina, H; J Immunol 1995, V154, P5426 HCAPLUS
(36) Molina, H; Proc Natl Acad Sci USA 1996, V93, P3357 HCAPLUS
(37) Nemerow, G; J Virol 1989, V63, P347 HCAPLUS
(38) Nichols, A; Proteins 1991, V11, P281
(39) Ohler, W; Ann Rheum Dis 2000, V59, P441 MEDLINE
(40) Prodeus, A; Immunity 1997, V7, P721 HCAPLUS
(41) Prodinger, W; J Immunol 1998, V161, P4604 HCAPLUS
(42) Qin, D; J Immunol 1998, V161, P4549 HCAPLUS
(43) Seyfield, R; Clin Exp Immunol 1997, V109, P480 HCAPLUS
(44) Szakonyi, G; Science 2001, V292, P1725 HCAPLUS
(45) Takahashi, K; J Immunol 1997, V159, P1857 HCAPLUS
(46) Tanner, J; Cell 1987, V50, P293 HCAPLUS
(47) Tedder, T; J Immunol 1994, V153, P4774 HCAPLUS
(48) Thornton, B; J Immunol 1994, V152, P1914 HCAPLUS
(49) Tsokos, G; Immunol Today 1998, V14, P56 HCAPLUS
(50) Weis, J; Proc Natl Acad Sci USA 1984, V81, P881 HCAPLUS
(51) Wilsen, J; Arthritis Rheum 1998, V41, P1111 MEDLINE
(52) Wu, X; J Immunol 2000, V165, P2116 HCAPLUS

L[illegible] ANSWER [illegible] OF [illegible] HCAPLUS COPYRIGHT [illegible] ACS
AN [illegible] HCAPLUS
DN [illegible]
TI **Structure** of **complement receptor 2** in complex with its C3d ligand
AU Szakonyi, Gerda; Guthridge, Joel M.; Li, Dawei; Young, Kendra; Holers, Michael; **Chen, Xiaojiang S.**
CS Department of Biochemistry and Molecular Genetics, University of Colorado Health Science Center, School of Medicine, Denver, CO, [illegible], USA
SO Science (Washington, D. C., United States) [illegible], [illegible], [illegible]
CODEN: SCIEAS; ISSN: [illegible]
PB American Association for the Advancement of Science
DT Journal
LA English
CC 15-4 (Immunochemistry)
Section cross-reference(s): 75
AB **Complement receptor 2** (**CR2**/CD21) is an important receptor that amplifies B lymphocyte activation by bridging the innate and adaptive immune systems. **CR2** ligands include complement C3d and Epstein-Barr virus glycoprotein 350/220. We describe the **x-ray** structure of this **CR2** domain in complex with C3d at 2.0 angstroms. The structure reveals extensive main chain interactions between C3d and only one short consensus repeat (SCR) of **CR2** and substantial SCR side-side packing. These results provide a detailed understanding of receptor-ligand interactions in this protein family and reveal potential target sites for **mol.** drug design.
ST **crystal** structure complement C3d **CR2** receptor complex
IT **Structure-activity relationship**
(complement receptor **CR2**-binding; of complement C3d)
IT **Structure-activity relationship**
(complement C3d-binding; of **complement receptor 2**)
IT **Crystal structure**
(**crystal** structure of **complement receptor 2** in complex with its C3d ligand)
IT **Hydrogen bond**
Molecular association
(interaction of **complement receptor 2** with complement C3d)
IT **Complement receptors**
RL: PRP (Properties)
(**type 2**, complex with complement C3d; **crystal** structure of **complement receptor 2** in complex with its C3d ligand)
IT [illegible]-45-0, complement C3d, complex with receptor
RL: PRP (Properties)
(**crystal** structure of **complement receptor 2** in complex with its C3d ligand)
IT [illegible] 40-3, Complement C3d
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study ; PROC (Process)
(interaction of **complement receptor 2** with complement C3d)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Ahearn, J; Immunity 1996, V4, P251 HCAPLUS
(2) Anon; www.scier.cemag.org/cgi/content/full/292/5522/1025/DC1
(3) Aubry, J; Nature 1992, V358, P505 HCAPLUS
(4) Barlow, P; J Mol Biol 1993, V232, P268 HCAPLUS
(5) Bjorkman, P; Nature 1997, V387, P1 HCAPLUS
(6) Brandon, C; Introduction to Protein Structure 1999, P1
(7) Brunger, A; Acta Crystallogr 1998, V54, P905 HCAPLUS

(8) [illegible]; Acta Crystallogr 1994, V50 , P760
(9) Carel, J; J Biol Chem 1990, V265, P12293 HCAPLUS
(10) Carter, R; Science 1992, V256, P118 HCAPLUS
(11) Casasnovas, J; EMBO J 1999, V18, P2911 HCAPLUS
(12) Clemenza, L; J Immunol 2000, V165, P3453 HCAPLUS
(13) Fearon, D; Semin Immunol 1995, V7, P350 HCAPLUS
(14) Fingeroth, J; Proc Natl Acad Sci 1984, V81, P4510 HCAPLUS
(15) Guthridge, J; Biochemistry in press
(16) Hebell, T; Science 1991, V254, P102 HCAPLUS
(17) Kalli, K; J Immunol 1991, V147, P844 HCAPLUS
(18) Law, S; Focus Series 1988
(19) Lowell, C; J Exp Med 1989, V170, P1931 HCAPLUS
(20) Martin, D; J Virol 1994, V68, P4710 HCAPLUS
(21) Moir, S; J Exp Med 2000, V192, P637 HCAPLUS
(22) Molina, H; J Immunol 1995, V154, P5426 HCAPLUS
(23) Molina, H; Proc Natl Acad Sci 1996, V93, P3357 HCAPLUS
(24) Nagar, B; Science 1998, V280, P1277 HCAPLUS
(25) Poznansky, M; J Immunol 1989, V143, P1254 HCAPLUS
(26) Prodeus, A; Immunity 1998, V9, P721 HCAPLUS
(27) Prodinger, W; J Immunol 1998, V161, P4604 HCAPLUS
(28) Rao, P; Cell Immunol 1985, V93, P549 MEDLINE
(29) Schwarzenbacher, R; EMBO J 1999, V18, P6228 HCAPLUS
(30) Wiles, A; J Mol Biol 1997, V272, P253 HCAPLUS

L63 ANSWER 4 OF 10 HCAPLUS
AN **2001:303769** HCAPLUS
DN **135:91271**
TI **Structural** Studies in Solution of the Recombinant N-Terminal Pair of Short Consensus/Complement Repeat Domains of **Complement Receptor Type 2** (**CR2**/CD21) and Interactions with Its Ligand C3dg
AU Guthridge, Joel M.; Rakstang, Jonathan K.; Young, Kendra A.; Hinshelwood, Justin; Aslam, Mohammed; Robertson, Alexis; Gipson, Matthew G.; Sarrias, Maria-Rosa; Moore, William T.; Meagher, Michael; Karp, David; Lambris, John D.; Perkins, Stephen J.; **Holers, V. Michael**
CS Departments of Medicine and Immunology Division of Rheumatology, University of Colorado Health Sciences Center, Denver, CO, 80262, USA
SO Biochemistry (2001), 40(20), 5931-5941
CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
CC 16-4 (Immunochemistry)
AB Human **complement receptor type 2** (**CR2**, CD21) is a cell surface receptor that binds three distinct ligands (complement C3d, Epstein-Barr virus gp350/220, and the low-affinity IgE receptor CD23) via the N-terminal two of fifteen or sixteen short consensus/complement repeat (SCR) domains. Here, we report biophys. studies of the **CR2** SCR 1-2 domain binding to its ligand C3dg. Two recombinant forms of **CR2** containing the first two and SCR 1-15 domains were expressed in high yield in Pichia pastoris and baculovirus, resp. CD spectroscopy showed that **CR2** SCR 1-2 receptor possessed a .beta.-sheet secondary structure with a melting temp. of 59 .degree.C. Using surface plasmon resonance, kinetic parameters for the binding of either **CR2** SCR 1-2 or the full-length SCR 1-15 form of **CR2** showed that the affinity of binding to immobilized C3d is comparable for the SCR 1-15 compared to the SCR 1-2 form of **CR2**. Unexpectedly, both the assocn. and dissocn. rates for the SCR 1-15 form were slower than for the SCR 1-2 form. These data show that the SCR 1-2 domains account for the primary C3dg binding site of **CR2** and that the distal SCR domains of full-length **CR2** influence the ability of **CR2** SCR 1-2 to interact with its ligand. Studies of the pH and ionic strength dependence of the

interaction between SCR 1-2 and 3d by surface plasmin resonance showed that this is influenced by charged interactions, possibly involving the sole His residue in **CR2** SCR 1-2. Sedimentation equil. studies of **CR2** SCR 1-2 gave **mol.** wts. of 17,[illegible], in good agreement with its sequence-derived **mol.** wt. to show that this was monomeric. Its sedimentation coeff. was deta. to be 1.36 S. The complex with C3d gave **mol.** wts. in 75 mM and 150 mM NaCl buffer that agreed closely with its sequence-derived **mol.** wt. of 57,[illegible] and showed that a 1:1 complex had been formed. **Mol.** graphics views of homol. models for the s-p. **CR2** SCR 1 and SCR 2 domains showed that both SCR domains exhibited a distribution of charged groups throughout its surface. The single His residue is located near a long eight-residue linker between the two SCR domains and may influence the linker conformation and the assocn. of C3d and **CR2** SCR 1-2 into their complex. Sedimentation modeling showed that the arrangement of the two SCR domains in **CR2** SCR 1-2 is highly extended in soln.

ST complement receptor CD2 interaction C3dg structure

IT Glycoproteins, specific or class
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(gp350/220, Epstein-Barr virus; soln. structure of the recombinant N-terminal pair of short consensus/complement repeat domains of **complement receptor type 2** (**CR2**/CD21) and interactions with C3dg and with)

IT **Conformation**
(protein; soln. structure of the recombinant N-terminal pair of short consensus/complement repeat domains of **complement receptor type 2** (**CR2**/CD21) and interactions with C3dg)

IT **Molecular association**
Molecular modeling
Secondary structure
.beta.-Sheet
(soln. structure of the recombinant N-terminal pair of short consensus/complement repeat domains of **complement receptor type 2** (**CR2**/CD21) and interactions with C3dg)

IT **Complement receptors**
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(**type 2**; soln. structure of the recombinant N-terminal pair of short consensus/complement repeat domains of **complement receptor type 2** (**CR2**/CD21) and interactions with C3dg)

IT 82903-93-3, complement c3dg
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(soln. structure of the recombinant N-terminal pair of short consensus/complement repeat domains of **complement receptor type 2** (**CR2**/CD21) and interactions with C3dg)

IT 80295-49-0, complement c3d
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(soln. structure of the recombinant N-terminal pair of short consensus/complement repeat domains of **complement receptor type 2** (**CR2**/CD21) and interactions with C3dg and with)

RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

(1) Ahearn, J; Adv Immunol 1989, V46, P1-38 HCAPLUS

(2) Ahearn, J; Immunity 1994, V1, P987 HCAPLUS

(3) Ahearn, J; Proc Natl Acad Sci U S A 1988, V85, P7793-7 HCAPLUS

(4) Ashton, A; J Mol Biol 1987, V[illegible], P4 HCAPLUS
(5) Aubry, J; J Immunol 1994, V152, P5405 HCAPLUS
(6) Aubry, J; Nature 1992, V358, P505 HCAPLUS
(7) Barlow, P; J Mol Biol 1993, V232, P268 HCAPLUS
(8) Blom, A; J Biol Chem 1999, V274, P19237 HCAPLUS
(9) Blom, A; J Immunol 2000, V164, P5625 HCAPLUS
(10) Bouma, B; EMBO J 1999, V18, P5166 HCAPLUS
(11) Carel, J; J Biol Chem 1990, V265, P12293 HCAPLUS
(12) Carel, J; J Immunol 1994, V153, P4379 HCAPLUS
(13) Carroll, M; Curr Opin Immunol 1998, V10, P36 HCAPLUS
(14) Carter, R; Science 1992, V256, P105 HCAPLUS
(15) Casanovas, J; EMBO J 1999, V18, P2911
(16) Clemenza, L; J Immunol 2000, V165, P3839 HCAPLUS
(17) Cohen, B; DNA 1986, V5, P239 HCAPLUS
(18) de Bruijn, M; Proc Natl Acad Sci U S A 1985, V82, P708 HCAPLUS
(19) Delcayre, A; EMBO J 1991, V10, P919 HCAPLUS
(20) Dempsey, P; Science 1996, V271, P348 HCAPLUS
(21) Drake, A; Methods in Molecular Biology 1994, P219 HCAPLUS
(22) Hedrick, J; J Immunol 1994, V153, P4419 HCAPLUS
(23) Holmskov, U; Adv Immunol 1999, V45, P381 HCAPLUS
(24) Kabsch, W; Biopolymers 1983, V22, P2577 HCAPLUS
(25) Kirkitadze, M; Biochem J 1998, V334, P167 HCAPLUS
(26) Kirkitadze, M; Biochemistry 1999, V38, P7019 HCAPLUS
(27) Laskowski, R; J Appl Crystallogr 1993, V26, P283 HCAPLUS
(28) Lee, B; J Mol Biol 1971, V55, P379 HCAPLUS
(29) Lowell, C; J Exp Med 1989, V170, P1931 HCAPLUS
(30) Martin, D; J Exp Med 1991, V174, P1299 HCAPLUS
(31) Martin, D; J Virol 1994, V68, P4716 HCAPLUS
(32) Molina, H; J Biol Chem 1991, V266, P11173 HCAPLUS
(33) Molina, H; J Immunol 1994, V153, P3589 HCAPLUS
(34) Molina, H; J Immunol 1995, V154, P5426 HCAPLUS
(35) Molina, H; Proc Natl Acad Sci U S A 1996, V93, P3357 HCAPLUS
(36) Moore, M; J Biol Chem 1989, V264, P20476 HCAPLUS
(37) Nagar, B; Science 1996, V271, P1777 HCAPLUS
(38) Nemerow, G; Cell 1989, V56, P369 HCAPLUS
(39) Nemerow, G; J Virol 1986, V58, P347 HCAPLUS
(40) Nemerow, G; J Virol 1985, V54, P347 HCAPLUS
(41) Pepys, M; J Exp Med 1974, V140, P126 MEDLINE
(42) Perkins, S; Biochem J 1993, V295, P87 HCAPLUS
(43) Perkins, S; Eur J Biochem 1986, V157, P169 HCAPLUS
(44) Pnillo, J; Anal Biochem 2000, V279, P151 HCAPLUS
(45) Provencher, S; Comput Phys Commun 1982, V27, P213
(46) Rao, P; Cell Immunol 1985, V93, P549 MEDLINE
(47) Sali, A; J Mol Biol 1990, V212, P403 HCAPLUS
(48) Smith, K; Biochem J 1990, V267, P203 HCAPLUS
(49) Stratton, J; Pichia Protocols 1998, P107 HCAPLUS
(50) Takeshita, S; Gene 1986, V71, P9 HCAPLUS
(51) Tedder, T; Immunol Today 1994, V15, P437 HCAPLUS
(52) Tedder, T; J Immunol 1994, V153, P4974 HCAPLUS
(53) Tessier, D; Gene 1991, V98, P177 HCAPLUS
(54) Weis, J; Proc Natl Acad Sci U S A 1984, V81, P881 HCAPLUS
(55) Zhang, W; Biotechnol Bioeng 2000, V70, P1 HCAPLUS

L63 ANSWER 5 OF 10 HCAPLUS COPYRIGHT 2002 ACS
AN 1999:602199 HCAPLUS
DN 132:166714
TI The **structural** basis for **complement receptor type 2 CR2**, CD21-mediated alternative pathway activation of complement: studies with **CR2** deletion mutants and vaccinia virus complement-control protein-**CR2** chimeras
AU Johnson, Anna Marina; Rosenblum, Aviella Miriam; Cui, F; Fleming, Ahearn, Joseph Michael; Lesley, Robert Graham, Hilton

CS Dep. Immunology Microbiology, Institute Medical Biology, Univ. Southern Denmark, Odense, DK-5000, Den.
SO European Journal of Immunology, 1998, [illegible], 3437-3444
CODEN: EJIMAF; ISSN: 0014-2980
PB Wiley-VCH Verlag GmbH
DT Journal
LA English
CC 15-4 (Immunochemistry)
AB The role of **complement receptor 2** (**CR2**) short consensus repeats (SCR) in binding of hydrolyzed C3 (iC3) to form an alternative pathway (AP) convertase, and promoting C3 fragment deposition following AP activation, was examd. The authors used (1) K562 cells transfected with **CR2** constructs, where the C3d-binding site of **CR2** (SCR1-2) was replaced with the 4-SCR vaccinia virus complement control protein (VCP), or truncation mutants thereof, and (2) COS cells transfected with wild-type (wt) **CR2**, or deletion mutants thereof. AP activation required iC3 binding in both systems. Thus, the VCP-**CR2** chimera had an iC3 binding efficiency of 11.4%, compared to wtCR2, and a relative AP activity of 5.59%, the truncation mutants being inactive. Of the **CR2** mutants, only EK (.DELTA.SCR1-11) had AP activity similar to wtCR2. NN (.DELTA.SCR6-8) and NCP (.DELTA.SCR6-mid14) had reduced AP activity, but near normal iC3 binding. XB (.DELTA.SCR3-6) and PP (.DELTA.SCR3-mid14) were inactive in both assays. The authors conclude that, while iC3 binding to **CR2** via SCR1-4 is essential for AP activation, the efficiency of C3 deposition also depends on the midportion of **CR2**.

ST **CR2** receptor short consensus repeat complement C3

IT Complement
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(alternative pathway; role of **complement receptor 2** (**CR2**) short consensus repeats in binding of complement iC3 to form an alternative pathway convertase)

IT **Structure-activity relationship**
(complement-activating; role of **complement receptor 2** (**CR2**) short consensus repeats in binding of complement iC3 to form an alternative pathway convertase)

IT **Protein motifs**
(short consensus repeats; role of **complement receptor 2** (**CR2**) short consensus repeats in binding of complement iC3 to form an alternative pathway convertase)

IT **Complement receptors**
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(**type 2**; role of **complement receptor 2** (**CR2**) short consensus repeats in binding of complement iC3 to form an alternative pathway convertase

IT 93829-19-3, Complement C3i
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(role of **complement receptor 2** (**CR2**) short consensus repeats in binding of complement iC3 to form an alternative pathway convertase)

IT 80295-67-6, Alternative complement pathway C3(C5) convertase
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(role of **complement receptor 2** (**CR2**) short consensus repeats in binding of complement iC3 to form an alternative pathway convertase)

RE
(1) Budeke, D; Cell Immunol 1974, V11, P1 MEDLINE
(2) Christensen, J; J Immunol Methods 1979, V28, P11
(3) Esparza, I; Eur J Immunol 1981, V11, P778 HCAPLUS
(4) Gallick, T; Current Protocols in Molecular Biology 1994, P2.1
(5) Kalli, K; J Immunol 1991, V147, P590 HCAPLUS
(6) Law, S; J Immunol 1979, V122, P759 HCAPLUS
(7) Leslie, R; Immunology 1998, V97, P371 HCAPLUS
(8) Lowell, C; J Exp Med 1989, V170, P1501 HCAPLUS
(9) Marquart, H; Clin Exp Immunol 1995, V101, P87 MEDLINE
(10) Marquart, H; J Immunol 1984, V133, P417 HCAPLUS
(11) McConnel, I; Eur J Immunol 1978, V8, P438
(12) McKenzie, R; J Infect Dis 1992, V166, P1245 HCAPLUS
(13) Mold, C; J Immunol 1986, V140, P1923 HCAPLUS
(14) Olesen, E; Immunology 1998, V93, P177 HCAPLUS
(15) Prat, F; Blood 1984, V63, P463 HCAPLUS
(16) Ramos, O; Proc Natl Acad Sci USA 1995, V92, P5470 MEDLINE
(17) Sahu, A; J Immunol 1998, V161, P3596 HCAPLUS
(18) Schwendinger, M; J Immunol 1997, V158, P5488 HCAPLUS
(19) Toye, P; J Immunol Methods 1995, V187, P95 HCAPLUS

L63 ANSWER 6 OF 10 HCAPLUS COPYRIGHT 2002 ACS
AN **1998:701309** HCAPLUS
DN **130:65005**
TI Characterization of C3dg binding to a recess formed between short consensus repeats 1 and 2 of **complement receptor type 2** (**CR2**; CD21)
AU Prodinger, Wolfgang M.; Schwendinger, Michael G.; Schoch, Jurgen; Koehle, Maria; Larcher, Clara; Dierich, Manfred P.
CS Institut fur Hygiene, University of Innsbruck, Innsbruck, Austria
SO Journal of Immunology (1998), 161(9), 4604-4610
CODEN: JOIMA3; ISSN: 0022-1767
PB American Association of Immunologists
DT Journal
LA English
CC 15-4 (Immunochemistry)
AB To allow for a better characterization of the ligand binding structures of human **complement receptor type 2** (**CR2**; CD21), we have established an IgG1 .kappa. mouse mAb, FE8, that interferes efficiently with binding of complement C3dg and EBV to **CR2**. In contrast to mAb OKB7, the only well-characterized mAb with similar specificity, mAb FE8 blocked binding of sol. C3dg or particles carrying multiple copies of surface-bound C3dg to **CR2** or induced complete removal of these ligands from the receptor. In vitro EBV infection of B lymphocytes, on the other hand, was abrogated by mAbs FE8 and OKB7 with similar dose-response characteristics. As FE8 was shown to recognize a discontinuous epitope, a series of overlapping peptides derived from SCR1 and -2 and immobilized on cellulose was screened with FE8. The results suggest that up to five discontinuous sequences contributed to the epitope. The sequence 65-EPPKHG-69, located between the two SCR units, reacted most intensively. Two other sequences, 16-YYGTTI-21 and 105 NGNKCVWGQPNN-116, are located between Cys and Cys of SCR1 and around Cys of SCR2, resp. Based on the soln. structure for two factor H SCRs, a **three-dimensional** model of SCR1 and -2 was generated. The FE8 binding peptide sequences were located in relative proximity to each other, bounding the recess formed between SCR1 and -2. This potential of mAb FE8 is currently unique and may be exploited for interfering with conditions of unwanted recognition of C3dg-coated structures by the immune system.
IT **Complement** C3dg binding **receptor type 2**, **complement receptor 2**
IT Cell proliferation
(B cell; characterization of **complement** C3dg binding **receptor type 2** by mAb FE8 and its effect on)

between short consensus repeats 1 and 2 of **complement receptor type 2**

IT Immunoglobulins
RL: ARG (Analytical reagent use); BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(G1, monoclonal; characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2** studied with

IT **Molecular association**
Protein sequences
Simulation and Modeling, biological
Tertiary structure
(characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2**)

IT Peptides, biological studies
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); PROC (Process)
(characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2**)

IT Immune system
(characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2** in relation to recognition by)

IT Epitopes
(conformational; characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2**)

IT Epitopes
(mapping; characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2**)

IT Human herpesvirus 4
(monoclonal Ig to C3dg inhibition of B cell transformation by)

IT Transformation, neoplastic
(monoclonal Ig to C3dg inhibition of B cell transformed by Epstein-Barr virus)

IT **Structure-activity relationship**
(peptide-binding; characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2**)

IT B cell (lymphocyte)
(proliferation; characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2**)

IT **Quaternary structure**
(protein; characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2**)

IT **Repeat motifs (protein)**
(short consensus; characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2**)

IT **Complement receptors**
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); IMF (Preparation); BIOL (Biological study); PROC (Process)
(**type 2**; characterization of complement C3dg

binding to recess formed between short consensus repeats 1 and 2 of
complement receptor type 2

IT [illegible]-93-[illegible], Complement C3dg
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2**)

IT [illegible]-97-1P [illegible] [illegible] [illegible] [illegible]
218129-01-2P 218129-03-4P 218129-04-5P 218129-05-6P 218129-[illegible]-7P
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); PROC (Process)
(characterization of complement C3dg binding to recess formed between short consensus repeats 1 and 2 of **complement receptor type 2**)

RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

(1) Aubry, J; J Immunol 1994, V152, P5806 HCAPLUS
(2) Barlow, P; Biochemistry 1991, V30, P997 HCAPLUS
(3) Barlow, P; J Mol Biol 1993, V23[illegible], P26[illegible] HCAPLUS
(4) Berger, P; Endocrinology 1988, V123, P2351 HCAPLUS
(5) Bohnsack, J; J Immunol 1988, V141, P2569 HCAPLUS
(6) Bonnefoy, J; Eur J Immunol 1993, V23, P969 HCAPLUS
(7) Carter, R; J Immunol 1989, V143, P17[illegible] HCAPLUS
(8) Carter, R; Science 1992, V256, P105 HCAPLUS
(9) Delibrias, C; J Immunol 1992, V149, P768 HCAPLUS
(10) Dempsey, P; Science 1996, V271, P348 HCAPLUS
(11) Fazekas, d; J Immunol Methods 1980, V35, P1
(12) Fearon, D; Annu Rev Immunol 1995, V13, P127 HCAPLUS
(13) Fischer, E; J Immunol 1991, V146, P86[illegible] HCAPLUS
(14) Frank, R; Tetrahedron 1988, V44, P9217 HCAPLUS
(15) Gasque, P; J Immunol 1996, V156, P2247 HCAPLUS
(16) Griffiten, A; Clin Immunol Immunopathol 1993, V69, P1 HCAPLUS
(17) Henchoz, S; Immunology 1994, V81, P285 HCAPLUS
(18) Hoffman, G; Proc Natl Acad Sci USA 1980, V77, P2979 HCAPLUS
(19) Janatova, J; Methods Enzymol 1988, V162, P579 HCAPLUS
(20) Kearney, J; J Immunol 1979, V123, P1548 MEDLINE
(21) Kinoshita, T; Int Immunol 1990, V2, P651 MEDLINE
(22) Lowell, C; J Exp Med 1989, V170, P1931 HCAPLUS
(23) Luxembourg, A; J Immunol 1994, V153, P4448 HCAPLUS
(24) Martin, D; J Exp Med 1991, V174, P1299 HCAPLUS
(25) Martin, D; J Virol 1994, V68, P4716 HCAPLUS
(26) Matsumoto, A; J Exp Med 1991, V173, P55 HCAPLUS
(27) Miller, G; Proc Natl Acad Sci USA 197[illegible], V70, P190
(28) Molina, H; J Biol Chem 1991, V266, P1[illegible] HCAPLUS
(29) Molina, H; J Immunol 1995, V154, P542[illegible] HCAPLUS
(30) Moore, M; J Biol Chem 1989, V264, P20576 HCAPLUS
(31) Nemerow, G; Cell 198[illegible], V[illegible], P369 HCAPLUS
(32) Nemerow, G; J Immunol 1981, V127, P272 MEDLINE
(33) Nemerow, G; J Immunol 198[illegible], V1[illegible], P3068 HCAPLUS
(34) Nemerow, G; J Virol 1985, V55, P347 HCAPLUS
(35) Norman, D; J Mol Biol 1991, V219, P717 HCAPLUS
(36) Pascual, J; J Immunol 1988, V141, P3869 HCAPLUS
(37) Pramoonjago, P; Int Immunol 1993, V5, P337 HCAPLUS
(38) Prodinger, W; Biochem J 1998, V331, P41 HCAPLUS
(39) Prodinger, W; Immunopharmacology 1997, V38, P141 HCAPLUS
(40) Prodinger, W; J Immunol 1996, V15[illegible], P[illegible] HCAPLUS
(41) Rao, P; Cell Immunol 1985, V9[illegible], P[illegible] MEDLINE
(42) Reid, K; Immunol Today 19[illegible], V1[illegible], P[illegible] MEDLINE
(43) Reljic, R; Eur J Immunol 1997, V27, P[illegible] HCAPLUS
(44) Reynes, M; J Immunol 19[illegible], V1[illegible], P[illegible] HCAPLUS

(45) Schwendinger, M; J Immunol 1989, V143, P3469 HCAPLUS
(46) Tedder, T; J Immunol 1994, V153, P4667 HCAPLUS
(47) Tsokos, G; Eur J Immunol 1986, V16, P1232 MEDLINE
(48) Vik, D; J Immunol 1988, V141, P2871 HCAPLUS
(49) Weis, J; J Exp Med 1988, V167, P1047 HCAPLUS
(50) Wilson, B; Blood 1985, V66, P864 HCAPLUS

L66 ANSWER 7 OF 10 HCAPLUS COPYRIGHT 2011 ACS
AN 1998:525993 HCAPLUS
DN 129:94222
TI **X-ray crystal structure** of C3d: a C3 fragment and ligand for **complement receptor 2**
AU Nagar, Bhushan; Jones, Russell G.; Diefenbach, Russell J.; Isenman, David E.; Rini, James M.
CS Department Biochemistry, Molecular Medical Genetics, University Toronto, Toronto, ON, M5S 1A8, Can.
SO Science (Washington, D. C.) (1998), 280(5367), 1277-1281
CODEN: SCIEAS; ISSN: 0036-8075
PB American Association for the Advancement of Science
DT Journal
LA English
CC 15-4 (Immunochemistry)
Section cross-reference(s): 75
AB Activation and covalent attachment of complement component C3 to pathogens is the key step in complement-mediated host defense. Addnl., the antigen-bound C3d fragment interacts with **complement receptor 2** (**CR2**; also known as CD21) on B cells and thereby contributes to the initiation of an acquired humoral response. The **x-ray crystal** structure of human C3d solved at 2.0 angstroms resoln. reveals an .alpha.-.alpha. barrel with the residues responsible for thiolester formation and covalent attachment at one end and an acidic pocket at the other. The structure supports a model whereby the transition of native C3 to its functionally active state involves the disruption of a complementary domain interface and provides insight into the basis for the interaction between C3d and **CR2**.
ST **crystal** structure complement C3d; **complement receptor 2** complement C3 interaction; receptor CD21 ligand complement C3 interaction
IT **Crystal structure**
(**crystal** structure of complement C3d (a C3 fragment) in relation to interaction between C3d and **complement receptor 2**)
IT **Conformation**
(protein; **crystal** structure of complement C3d (a C3 fragment) in relation to interaction between C3d and **complement receptor 2**)
IT **Complement receptors**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**type 2**; **crystal** structure of complement C3d (a C3 fragment) in relation to interaction between C3d and **complement receptor 2**)
IT 80295-41-6, Complement C3 80295-42-7, Complement C3d
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(**crystal** structure of complement C3d (a C3 fragment) in relation to interaction between C3d and **complement receptor 2**)

L66 ANSWER 8 OF 10 HCAPLUS COPYRIGHT 2011 ACS
AN **1995:548776** HCAPLUS
DN **122:312636**

TI Characterization of a **complement receptor 2** (**CR2**, CD21) ligand binding site for C3. An initial model of ligand interaction with two linked short consensus repeat modules

AU Molina, Hector; Perkins, Stephen J.; Sutthidge, Joel; Hinks, John; Kinoshita, Taroh; **Holers, V. Michael**

CS Dep. of Medicine, Washington Univ. Sch. of Medicine, St. Louis, MO, 63110, USA

SO Journal of Immunology (1990), 154(1), 541-8
CODEN: JOIMA3; ISSN: 0022-1767

PB American Association of Immunologists

DT Journal

LA English

CC 15-4 (Immunochemistry)

AB Human **CR2** (CD21, EBV receptor) is an approx. 140-kDa receptor and a member of the regulators of complement activation gene family. Regulators of complement activation proteins are characterized by the presence of repeating motifs of 60 to 70 amino acids that are designated short consensus repeats (SCR). **CR2** serves as a receptor for four distinct ligands. Three of these ligands (complement C3, gp350/220 of EBV, and CD23) interact with the amino terminal 2 of 16 SCR (SCR 1 and 2). Previous studies have detd. that at least four sites are important in allowing **CR2** to efficiently bind EBV. Two of these sites are also important for binding mAb OKB7, a reagent that blocks both EBV and iC3b/C3dg binding to **CR2** chimeras, a rat anti-mouse **CR2** mAb designated 4E3 that blocks receptor binding to C3, and human **CR2**-derived peptides. In addn. to demonstrating an important role for the same sequence in SCR 1 that is part of the mAb OKB7 and EBV binding site, we have identified a new region within SCR 2 that interacts with C3. These results, when compared with a model of a dual SCR soln. structure derived from human factor H SCR, predict that two distinct largely surface-exposed sites on **CR2** interact with iC3b. A relative twist of 130.degree. about the long **axis** of the second SCR in this model would be necessary for these sites to form a single patch for iC3b binding on **CR2**.

ST complement receptor **CR2** binding site

IT **Complement receptors**
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(characterization of complement receptor **CR2** ligand-binding site for complement C3)

IT **Molecular structure-biological activity relationship**
(complement C3-binding; of complement receptor **CR2**)

IT **Receptors**
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(**CR2** (**complement receptor type 2**), characterization of **complement receptor CR2** ligand-binding site for **complement** C3)

IT **Receptors**
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(**complement**, characterization of **complement receptor CR2** ligand-binding site for **complement** C3)

IT 80295-41-6, Complement C3 80604-53-1, Complement iC3b
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(characterization of complement receptor **CR2** ligand-binding site for complement C3)

L61 ANSWER 9 OF 16 HCAPLUS COPYRIGHT 2004 ACS

AN 1990:513487 HCAPLUS

DN 113:113487

TI Structural requirements for C3d,g (protein-Epstein-Barr virus receptor) **CR2**

(CD21) ligand binding, internalization, and viral infection
AU Carel, Jean Claude; Myones, Barry L.; Frazier, Beth; **Holers, V. Michael**
CS Sch. Med., Washington Univ., St. Louis, MO, 63110, USA
SO Journal of Biological Chemistry (1989), 264(21), 12168-74
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
CC 15-4 (Immunochemistry)
AB The structure of **CR2**, the human C3d,g EBV receptor (**CR2** /CD21), consists of fifteen or sixteen 60-70 amino acid repeats called short consensus repeats (SCRs) followed by a transmembrane and a 34-amino acid intracytoplasmic domain. Functions of **CR2** include binding the human complement component C3d,g when it is covalently attached to targets or cross-linked in the fluid phase. In addn., **CR2** binds the Epstein-Barr virus (EBV) and mediates internalization of EBV and subsequent infection of cells. In order to explore functional roles of the repetitive extracytoplasmic SCR structure and the intracytoplasmic domain of **CR2**, the authors have created truncated **CR2** (rCR2) mutants bearing serial deletions of extracytoplasmic SCRs and also the intracytoplasmic tail. RCR2 mutants were transfected into two cell lines, murine fibroblast L cells and human erythroleukemic K562 cells. Phenotypic anal. of these expressed mutants revealed that the C3d,g- and EBV-binding sites are found in the two amino-terminal SCRs of **CR2** and expression of SCRs 1 and 4 is further required for high affinity binding to sol. cross-linked C3d,g. The intracytoplasmic domain of **CR2** is not required for binding C3d,g or EBV but is necessary to internalization of cross-linked C3d,g as well as for EBV infection of cells. Monoclonal anti-**CR2** antibodies with similar activities react with single widely sepd. epitopes, and no functional roles can yet be clearly assigned to SCRs 5-15, as rCR2 mutants not contg. these SCRs show no major differences from wild-type rCR2 in binding or internalizing cross-linked C3d,g or mediating EBV binding and infection.
ST Epstein Barr virus complement receptor structure; complement C3dg receptor structure function
IT **Receptors**
RL: BIOL (Biological study)
(for **complement** C3dg and Epstein-Barr virus, **CR2**, ligand binding and internalization and viral infection structural requirements of)
IT Antigens
RL: BIOL (Biological study)
(CD21, as complement C3dg and Epstein-Barr virus receptor, ligand binding and internalization and viral infection structural requirements of)
IT Virus, animal
(Epstein-Barr, complement receptor **CR2** for, binding and internalization and infection structural requirements of)
IT **Molecular structure-biological activity relationship**
(C3d,g-binding, of complement receptor **CR2**)
IT 82909-93-5, Complement C3d,g
RL: BIOL (Biological study)
(receptor for, **CR2**, ligand binding and internalization structural requirements of)

L63 ANSWER 10 OF 10 HCAPLUS COPYRIGHT 2002 ACS
AN 1989:22046 HCAPLUS
DN 110:22046
TI **Structure** of the human B lymphocyte receptor for C3d and the Epstein-Barr virus and relatedness to other members of the family of C3/4 binding proteins
AU Weis, Janis J.; Tedder, Thomas E.; Smith, Tim A.; Weis, John H.; Fearon, Douglas T.

CS Dep. Rheumatol. Immunol., Brigham and Women's Hosp., Boston, MA, 02115, USA
SO Journal of Experimental Medicine (1993), 177(4), 1047-56
CODEN: JEMEAV; ISSN: 0022-1007
DT Journal
LA English
CC 15-4 (Immunochemistry)
Section cross-reference(s): 3
AB Human **complement receptor type 2** (**CR2**) is the B lymphocyte receptor for C3d and the Epstein-Barr virus. Overlapping cDNA clones encoding the entire human **CR2** protein were isolated from a human tonsillar cDNA library. The derived amino acid sequence of 1,032 residues encodes a peptide of 112,716 **mol.** wt. A signal peptide was identified, followed by 15 copies of the short consensus repeat (SCR) structure common to the C3/C4-binding protein family. The entire extracellular portion of the protein comprised SCRs, thus, the ligand binding sites both for C3d and the EBV protein gp350/220 are positioned within this structure. Immediately following the final SCR was a transmembrane sequence of 24 amino acids and a cytoplasmic region of 34 amino acids. One of 5 cDNA clones isolated contained an addnl. SCR, providing evidence for alternative mRNA splicing or gene products of different human alleles. Anal. of the **CR2** cDNA sequence indicated that **CR2** contained internally homologous regions and suggested the **CR2** arose by duplication of a primordial gene sequence encoding 4 SCRs. Comparison of the **CR2** peptide sequence with those of other members of the gene family has identified many regions highly homologous with human CR1, fewer with C4bp and decay accelerating factor, and very few with factor H, and suggested that **CR2** and CR1 arose by duplication of the same ancestral gene sequence. The homol. between **CR2** and CR1 extended to the transmembrane and cytoplasmic regions, suggesting that these sequences were derived from a common membrane-bound precursor.
ST lymphocyte receptor complement C3d sequence; gene sequence receptor complement **CR2**
IT **Receptors**
RL: BIOL (Biological study)
(for **complement** C3d and Epstein-Barr virus, **CR2**, sequences of protein and gene for)
IT Protein sequences
(of complement receptor **CR2** precursor, of B lymphocyte of human, complete)
IT Protein sequences
(of complement receptor **CR2**, of B lymphocyte of human, complete)
IT Lymphocyte
(B-, complement receptor **CR2** of, gene and protein sequences of human)
IT Virus, animal
(Epstein-Barr, receptor for complement C3d and, sequences of protein and gene for)
IT **Deoxyribonucleic acid sequences**
(**complement receptor type 2** -specifying, of B lymphocyte of human, complete)
IT 118217-13-3 118217-14-4 118217-15-5 118217-16-6
RL: PRP (Properties)
(amino acid sequence of)
IT 80291-45-0, Complement C3d
RL: BIOL (Biological study)
(receptor for Epstein-Barr virus and, sequences of protein and gene for)
IT 118216-43-6, Deoxyribonucleic acid (human clone lambda.gt11 lambda.gt11 complement **3d** receptor membrane RNA-) (complementary)
118216-44-7, Deoxyribonucleic acid (human clone lambda.gt11 lambda.gt11

complement 3d receptor messenger RNA-complementary
RL: PRP (Properties
(sequence of

=> fil medline
FILE 'MEDLINE' ENTERED AT 11:3[illegible] ON [illegible]

FILE LAST UPDATED: [illegible]. FILE COVERS 1951 TO DATE.

On June 9, 2002, MEDLINE was reloaded. See HELP RELOAD for details.

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L93 ANSWER 1 OF 9 MEDLINE
AN **2002423637** MEDLINE
DN **22155856** PubMed ID: **12122212**
TI The crystal structure of human CD21: Implications for Epstein-Barr virus and C3d binding.
AU Prota Andrea E; Sage David R; Stehle Thilo; Fingeroth Joyce D
CS Harvard Medical School, Division of Experimental Medicine and Infectious Diseases, Beth Israel Deaconess Medical Center, Harvard Institutes of Medicine, 4 Blackfan Circle, Boston, MA 02115, USA.
NC AI45716 (NIAID)
DE13186 (NIDCR)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2002 Aug 6) 99 (16) 10641-6.
Journal code: [illegible]. ISSN: 0027-8424.
CY United States
DT Journal; Article; [illegible]
LA English
FS Priority Journals
EM 200209
ED Entered STN: 20020816
Last Updated on STN: [illegible]
Entered Medline: 20020923
AB Human **complement receptor type 2** (CD21) is the cellular receptor for Epstein-Barr virus (EBV), a human tumor virus. The N-terminal two short consensus repeats (SCR1-SCR2) of the receptor interact with the EBV glycoprotein gp[illegible] and also with the natural CD21 ligand C3d. Here we present the crystal structure of the SCR1-SCR2 fragment in the absence of ligand and demonstrate that it is

able to bind EBV. Based on a functional analysis of wild-type and mutant CD21 and molecular modelling, we identify a likely region for EBV attachment and demonstrate that this region is not involved in the interaction with C3d. A comparison with the previously determined structure of CD21 SCR1-SCR2 in complex with C3d shows that, in both cases, CD21 assumes compact Y-shaped conformations. However, our analysis reveals a surprising degree of flexibility at the SCR1-SCR2 interface, suggesting interactions between the two domains are not specific. We present evidence that the Y-shaped conformation is induced by deglycosylation of the protein, and that physiologic glycosylation of CD21 would result in a more extended conformation, perhaps with additional epitopes for C3d binding.

CT Check Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Carbohydrate Sequence
*Complement 3d: CH, chemistry
Complement 3d: IM, immunology
Crystallography, X-Ray
*Herpesvirus 4, Human: CH, chemistry
Herpesvirus 4, Human: IM, immunology
Models, Molecular
Molecular Sequence Data
***Receptors, Complement 3d: CH, chemistry**
Receptors, Complement 3d: GE, genetics
Receptors, Complement 3d: IM, immunology

RN 80295-45-0 (Complement 3d)
CN C (Receptors, Complement 3d)

L93 ANSWER 2 OF 9 MEDLINE
AN **2001662576** MEDLINE
DN **21555183** PubMed ID: **11698449**
TI Epitope mapping using the X-ray crystallographic structure of **complement receptor type 2** (**CR2**)/CD21: identification of a highly inhibitory monoclonal antibody that directly recognizes the **CR2**-C3d interface.
AU Guthridge J M; Young K; Gipson M G; Sarrias M R; Szakonyi G; Chen X S; Malaspina A; Donoghue E; James J A; Lambris J D; Moir S A; Perkins S C; **Holers V M**
CS Department of Medicine, University of Colorado Health Sciences Center, Denver, CO 80262, USA.
NC R0-1 AI36640 (NIAID)
R0-1 AR01681 (NIAMS)
R0-1 AR45954 (NIAMS)
R0-1 CA83615 (NCI)
SO JOURNAL OF IMMUNOLOGY, (2001 Nov 15) 167 (10) 5758-66.
Journal code: 2985117R. ISSN: 0022-1767.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 200112
ED Entered STN: 20011119
Last Updated on STN: 20020123
Entered Medline: 20011207
AB **Complement receptor type 2** (**CR2**)/CD21 is a B lymphocyte cell membrane C3d/iC3b receptor that plays a central role in the immune response. Human **CR2** is also the receptor for the EBV viral membrane glycoprotein gp350/220. Both C3d and gp350/220 bind **CR2** within the first two of 15-16 repetitive domains that have been designated short consensus/complement repeats. Many mAbs react with human **CR2**; however, only one currently available mAb is known to block both C3d/iC3b and gp350/220 binding. We have used a recombinant form of human **CR2** containing the short consensus/complement repeat 1-2 ligand-binding fragment to immunize **Cr2**(-/-) mice. Following fusion, we identified and further

characterized four new anti-**CR2** mAbs that recognize this fragment. Three of these inhibited binding of **CR2** to C3d and gp350/220 in different forms. We have determined the relative inhibitory ability of the four mAbs to block ligand binding, and we have used overlapping peptide-based approaches to identify linear epitopes recognized by the inhibitory mAbs. Placement of these epitopes on the recently solved crystal structure of the **CR2**-C3d complex reveals that each inhibitory mAb recognizes a site either within or adjacent to the **CR2**-C3d contact site. One new mAb, designated 7H1, blocks **CR2** receptor-ligand interactions with the greatest efficiency and recognizes a portion of the C3d contact site on **CR2**. Thus, we have created an anti-human **CR2** mAb that blocks the C3d ligand by direct contact with its interaction site, and we have provided confirmatory evidence that the C3d binding site seen in its crystal structure exists in solution.

CT Check Tags: Animal; Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
*Antibodies, Monoclonal: IM, immunology
Antigen-Antibody Complex: IM, immunology
Binding Sites
Binding, Competitive
Complement 3b: ME, metabolism
Complement 3d: IM, immunology
*Complement 3d: ME, metabolism
Crystallography, X-Ray
*Epitope Mapping
HIV-1: IM, immunology
Mice
Mice, Knockout
Models, Molecular
Peptide Fragments: ME, metabolism
***Receptors, Complement 3d: CH, chemistry**
Receptors, Complement 3d: IM, immunology
Receptors, Complement 3d: ME, metabolism
T-Lymphocytes: VI, virology
Viral Matrix Proteins: ME, metabolism

RN 81295-48-8 (Complement 3b); 80295-45-0 (Complement 3d)
CN 0 (Antibodies, Monoclonal); 0 (Antigen-Antibody Complex); 0 (EBV-associated membrane antigen); 0 (Peptide Fragments); 0 (Receptors, Complement 3d); 0 (Viral Matrix Proteins); 0 (complement 3d,g)

L93 ANSWER 3 OF 9 MEDLINE
AN **2001314375** MEDLINE
DN **21281281** PubMed ID: **11387479**
TI Structure of **complement receptor 2** in complex with its C3d ligand.
AU Szakonyi G; Guthridge J M; Li D; Young K; **Holers V M**; Chen X S
CS Department of Biochemistry and Molecular Genetics, University of Colorado Health Sciences Center, School of Medicine, Denver, CO 80262, USA.
NC R01-CA58615 (NCI)
SO SCIENCE, (2001 Jun 1) 292 (5522) 1725-8.
Journal code: 0404511. ISSN: 0036-8075.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS PDB-1GHQ
EM 200106
ED Entered STN: 20010702
Last Updated on STN: 20010702
Entered Medline: 20010628
AB **Complement receptor 2** (CR2/CD21) is an important receptor that amplifies B lymphocyte activation by

bridging the innate and adaptive immune systems. **CR2** ligands include complement C3d and Epstein-Barr virus glycoprotein 350. We describe the x-ray structure of this **CR2** domain in complex with C3d at 2.0 angstroms. The structure reveals extensive main chain interactions between C3d and only two short consensus repeat (SCR) of **CR2** and substantial SCR side-side packing. These results provide a detailed understanding of receptor-ligand interactions in this protein family and reveal potential target sites for molecular drug design.

CT Check Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Amino Acid Sequence
Antibodies, Monoclonal
Complement 3d: CH, chemistry
Complement 3d: GE, genetics
*Complement 3d: ME, metabolism
Consensus Sequence
Crystallography, X-Ray
Hydrogen Bonding
Ligands
Models, Molecular
Molecular Sequence Data
Mutagenesis
Protein Conformation
Protein Folding
Protein Sorting Signals
Protein Structure, Secondary
Protein Structure, Tertiary
***Receptors, Complement 3d: CH, chemistry**
Receptors, Complement 3d: IM, immunology
***Receptors, Complement 3d: ME, metabolism**
Recombinant Proteins: ME, metabolism

RN 80298-45-9 (Complement 3d)

CN 1 (Antibodies, Monoclonal); 0 (Ligands); 0 (Protein Sorting Signals); 0 (Receptors, Complement 3d); 0 (Recombinant Proteins)

L93 ANSWER 4 OF 9 MEDLINE

AN **2001293762** MEDLINE

DN **21250697** PubMed ID: **11352728**

TI Structural studies in solution of the recombinant N-terminal pair of short consensus/complement repeat domains of **complement receptor type 2** (**CR2**/CD21) and interactions with its ligand C3dg.

AU Guthridge J M; Rakstang J K; Young K A; Hinshelwood J; Aslam M; Robertson A; Gipson M G; Sarrias M R; Moore W T; Meagher M; Karp D; Lambris J D; Perkins S J; **Holers V M**

CS Department of Medicine, Division of Rheumatology, University of Colorado Health Sciences Center, Denver, Colorado 80262, USA.

NC CA16520 (NCI)
DK19525 (NIDDK)
RO-1 AI33943 (NIAID)
RO-1 CA55615 (NCI)

SO BIOCHEMISTRY, (2001 May 22) 40 (20) 5931-41.
Journal code: 0370623. ISSN: 0006-2960.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 200106

ED Entered STN: 20010620
Last Updated on STN: 20010820
Entered Medline: 20010615

AB Human **complement receptor type 2** (**CR2**, CD21) is a cell surface receptor that binds three distinct ligands (complement C3d, Epstein-Barr virus gp350/220, and the

low-affinity IgE receptor CD23 via the N-terminal two to fifteen to sixteen short consensus complement repeat (SCR) domains. Here, we report biophysical studies of the **CR2** SCR 1-2 domain binding to its ligand C3dg. Two recombinant forms of **CR2** containing the SCR 1-2 and SCR 1-15 domains were expressed in high yield in Pichia pastoris and baculovirus, respectively. Circular dichroism spectroscopy showed that **CR2** SCR 1-2 receptor possessed a beta-sheet secondary structure with a melting temperature of 54 degrees C. Using surface plasmon resonance, kinetic parameters for the binding of either **CR2** SCR 1-2 or the full-length SCR 1-15 form of **CR2** showed that the affinity of binding to immobilized C3d is comparable for the SCR 1-15 compared to the SCR 1-2 form of **CR2**. Unexpectedly, both the association and dissociation rates for the SCR 1-15 form were slower than for the SCR 1-2 form. These data show that the SCR 1-2 domains account for the primary C3dg binding site of **CR2** and that the additional SCR domains of full-length **CR2** influence the ability of **CR2** SCR 1-2 to interact with its ligand. Studies of the pH and ionic strength dependence of the interaction between SCR 1-2 and C3d by surface plasmon resonance showed that this is influenced by charged interactions, possibly involving the sole His residue in **CR2** SCR 1-2. Sedimentation equilibrium studies of **CR2** SCR 1-2 gave molecular weights of 17 000, in good agreement with its sequence-derived molecular weight to show that this was monomeric. Its sedimentation coefficient was determined to be 1.36 S. The complex with C3d gave molecular weights in 50 mM and 200 mM NaCl buffer that agreed closely with its sequence-derived molecular weight of 39 600 and showed that a 1:1 complex had been formed. Molecular graphics views of homology models for the separate **CR2** SCR 1 and SCR 2 domains showed that both SCR domains exhibited a distribution of charged groups throughout its surface. The single His residue is located near a long eight-residue linker between the two SCR domains and may influence the linker conformation and the association of C3d and **CR2** SCR 1-2 into their complex. Sedimentation modeling showed that the arrangement of the two SCR domains in **CR2** SCR 1-2 is highly extended in solution.

CT Check Tags: Comparative Study; Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Amino Acid Sequence
Binding, Competitive
Cloning, Molecular: MT, methods
*Complement 3b: ME, metabolism
Computer Simulation
Consensus Sequence
Ligands
Models, Molecular
Molecular Sequence Data
Peptide Fragments: BI, biosynthesis
*Peptide Fragments: CH, chemistry
*Peptide Fragments: ME, metabolism
Pichia: GE, genetics
Protein Binding
Receptors, Complement 3d: BI, biosynthesis
***Receptors, Complement 3d: CH, chemistry**
***Receptors, Complement 3d: ME, metabolism**
Recombinant Proteins: BI, biosynthesis
Recombinant Proteins: CH, chemistry
Recombinant Proteins: ME, metabolism
Repetitive Sequences, Amino Acid
Sequence Alignment
Solutions
Spectrometry, Mass, Matrix-Assisted Laser Desorption-Ionization
Structure-Activity Relationship
Surface Plasmon Resonance
Ultracentrifugation

RN 80295-45-1 Complement 3d
CN 0 (Ligands ; 1 Peptide Fragments ; 2 Receptors, Complement 3d ; 3 Recombinant Proteins ; 4 Synthetic ; 5 Complement 3d)

L96 ANSWER 5 OF 9 MEDLINE
AN **1998259089** MEDLINE
DN **98259089** PubMed ID: **9596584**
TI X-ray crystal structure of C3d: a C3 fragment and ligand for **complement receptor 2**.
AU Nagar B; Jones R G; Diefenbach R J; Isenman D E; Rini J M
CS Department of Biochemistry and Department of Molecular and Medical Genetics, University of Toronto, Toronto, Ontario, M5S 1A8, Canada.
SO SCIENCE, (1998 May 22) 280 [illegible] 1277-81.
Journal code: 0404511. ISSN: 0036-8075.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS PDB-UNKNOWN
EM 199806
ED Entered STN: 19980625
Last Updated on STN: 19980625
Entered Medline: 19980612
AB Activation and covalent attachment of complement component C3 to pathogens is the key step in complement-mediated host defense. Additionally, the antigen-bound C3d fragment interacts with **complement receptor 2** (**CR2**; also known as CD21) on B cells and thereby contributes to the initiation of an acquired humoral response. The x-ray crystal structure of human C3d solved at 2.0 angstroms resolution reveals an alpha-alpha barrel with the residues responsible for thioester formation and covalent attachment at one end and an acidic pocket at the other. The structure supports a model whereby the transition of native C3 to its functionally active state involves the disruption of a complementary domain interface and provides insight into the basis for the interaction between C3d and **CR2**.
CT Check Tags: Animal; Human; Support, Non-U.S. Gov't
Amino Acid Sequence
*Complement 3d: CH, chemistry
Complement 3d: ME, metabolism
Conserved Sequence
Crystallography, X-Ray
Ligands
Models, Molecular
Molecular Sequence Data
Mutation
Protein Conformation
Protein Structure, Secondary
***Receptors, Complement 3d: ME, metabolism**
Sequence Alignment
RN 80295-45-1 (Complement 3d)
CN 0 (Ligands); 1 (Receptors, Complement 3d)

L96 ANSWER 6 OF 9 MEDLINE
AN **95248110** MEDLINE
DN **95248110** PubMed ID: **7730644**
TI Characterization of a **complement receptor 2** (**CR2**, CD21) ligand binding site for C3. An initial model of ligand interaction with two linked short consensus repeat modules.
AU Molina H; Perkins S J; Guthridge J; Gorka J; Kinoshita T; **Holers V M**
CS Howard Hughes Medical Institute, Washington University School of Medicine, St. Louis, MO 63110, USA.
SO JOURNAL OF IMMUNOLOGY, (1995 May 1) 154 [illegible] 4426-35.

Journal code: [illegible]. ISSN: [illegible].
CY United States
DT Journal; Article; JOURNAL ARTICLE
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 199105
ED Entered STN: 19910616
Last Updated on STN: 19910616
Entered Medline: 19910531
AB Human **CR2** (CD21, EBV receptor) is an approximately 145-kDa receptor and a member of the Regulators of Complement Activation gene family. Regulators of complement activation proteins are characterized by the presence of repeating motifs of 61 to 71 amino acids that are designated short consensus repeats (SCR). **CR2** serves as a receptor for four distinct ligands. Three of these ligands (complement C3, gp350/220 of EBV, and CD23) interact with the amino terminal 2 of 16 SCR (SCR 1 and 2). Previous studies have determined that at least four sites are important in allowing **CR2** to efficiently bind EBV. Two of these sites are also important for binding mAb OKB7, a reagent that blocks both EBV and iC3b/C3dg binding to **CR2**. We have identified and characterized important sites of iC3b ligand binding by utilizing human-mouse **CR2** chimeras, a rat anti-mouse **CR2** mAb designated 4E9 that blocks receptor binding to C3, and human **CR2** -derived peptides. In addition to demonstrating an important role for the same sequence in SCR 1 that is part of the mAb OKB7 and EBV binding site, we have identified a new region within SCR 2 that interacts with C3. These results, when compared with a model of a dual SCR solution structure derived from human factor H SCR, predict that two distinct largely surface-exposed sites on **CR2** interact with iC3b. A relative twist of 130 degrees about the long axis of the second SCR in this model would be necessary for these sites to form a single patch for iC3b binding on **CR2**.
CT Check Tags: Animal; Comparative Study; Human
Amino Acid Sequence
Antibodies, Monoclonal: IM, immunology
Cell Line
Chimeric Proteins: CH, chemistry
Chimeric Proteins: ME, metabolism
*Complement 3b: ME, metabolism
Complement Factor H: CH, chemistry
DNA, Complementary: AN, analysis
Flow Cytometry
Magnetic Resonance Spectroscopy
Mice
Models, Molecular
Molecular Sequence Data
***Receptors, Complement 3d: CH, chemistry**
Receptors, Complement 3d: IM, immunology
***Receptors, Complement 3d: ME, metabolism**
Rosette Formation
Sequence Homology, Amino Acid
Sheep
RN [illegible] (Complement 3b); [illegible] (Complement Factor H)
CN 0 (Antibodies, Monoclonal); 0 (Chimeric Proteins); 0 (DNA, Complementary); 0 (Receptors, Complement 3d)

L96 ANSWER 7 OF 9 MEDLINE
AN **91170746** MEDLINE
DN **91170746** PubMed ID: **1706386**
TI Characterization of the human **complement receptor 2** (**CR2**, CD21) promoter reveals sequences shared with regulatory regions of other genes primarily restricted to B cells [illegible].
AU Ruyhel E J; DeHoff M H; **Holers V M**

IS Howard Hughes Medical Institute Laboratories, Department of Medicine, Washington University School of Medicine, St. Louis, MO 63110.
SO JOURNAL OF IMMUNOLOGY, 1991 Mar 15 146 6 2021-6.
Journal code: 2985117R. ISSN: 0022-1767.
CY United States
DT Journal; Article; JOURNAL ARTICLE
LA English
FS Abridged Index Medicus Journals; Priority Journals
OS GENBANK-M37766
EM 199104
ED Entered STN: 19910515
Last Updated on STN: 19960129
Entered Medline: 19910422
AB Expression of human **complement receptor 2** (**CR2**, CD21, C3d,g/EBV receptor) is developmentally restricted on human B lymphocytes to cells of the late-pre and mature stages. **CR2** is also a member of the genetically linked regulators of complement activation family found on human chromosome 1q32. Regulators of complement activation proteins are variably expressed in plasma, on cell membranes, and in nonvascular extracellular fluid sites. To begin to understand the mechanisms that control both tissue specific and B cell developmental restriction of **CR2** expression, we have cloned and characterized the **CR2** promoter upstream of a single apparent transcriptional initiation site. Within this region are sequences with significant similarity to previously characterized TATA, SP1, AP-2, AP-1-like, and Ig enhancer E motif DNA protein binding sites, in addition to direct and inverted repeats. Significant regions of identity are also found between **CR2** promoter sequences and those of the CD23 promoter, another protein whose expression is developmentally restricted on B cells. The **CR2** promoter will direct transcription of the reporter gene chloramphenicol acyltransferase when transiently transfected into the human Raji B cell line. Therefore, we have identified the promoter for a human B cell protein whose expression is developmentally restricted. Further analysis of this region and the transcriptional regulation of **CR2** gene expression should lead to significant insights into the molecular mechanisms by which B cells mature and are activated.
CT Check Tags: Human; Support, Non-U.S. Gov't
*Antigens, CD: GE, genetics
Antigens, Differentiation, B-Lymphocyte: GE, genetics
*B-Lymphocytes: IM, immunology
Base Sequence
Gene Expression Regulation: GE, genetics
Molecular Sequence Data
Promoter Regions (Genetics): GE, genetics
RNA: BI, biosynthesis
***Receptors, Complement: GE, genetics**
Receptors, Complement 3d
RN 0 (RNA)
CN 0 (Antigens, CD); 0 (Antigens, Differentiation, B-Lymphocyte); 0 (Receptors, Complement); 0 (Receptors, Complement 3d)
GEN **CR2**; ECA

L93 ANSWER 8 OF 9 MEDLINE
AN **91010789** MEDLINE
IN **91010789** PubMed ID: **2145366**
TI A molecular and immunochemical characterization of mouse **CR2**. Evidence for a single gene model of mouse complement receptors 1 and 2.
AU Molina H; Kinoshita T; Inoue K; Carel J C; **Holers V M**
CS Howard Hughes Medical Institute Laboratories, Washington University School of Medicine, St. Louis, MO 63110.
SO JOURNAL OF IMMUNOLOGY, 1990 Nov 1 145 9 3004-9.
Journal code: 2985117R. ISSN: 0022-1767.

CY United States
DT Journal; Article; JOURNAL ARTICLE
LA English
FS Abridged Index Medicus Journals; Priority Journals
GS GENBANK-M61136
EM 199011
ED Entered STN: 19910117
Last Updated on STN: 19910117
Entered Medline: 19901101
AB The relationships between functional, biochemical, and genetic [illegible] of human and mouse C receptors 1 (CR1) and 2 (**CR2**) are incompletely understood. We have isolated and characterized a partial mouse **CR2** cDNA clone and determined the exon-intron organization of the gene encoding it. Together they predict a form of mouse **CR2** highly identical to the 15 short consensus repeat form of human **CR2**. Strong similarities in genomic organization and exon-intron junctions indicate that this mouse gene and human **CR2** are evolutionary homologues. A polyclonal rabbit anti-mouse **CR2** fusion protein, BRN-1, was prepared. BRN-1 immunoprecipitates bands of 155 to 160 kDa under nonreducing conditions in mouse **CR2** expressing B cell lines. In mouse spleen a doublet of 155 kDa and 190 kDa under nonreducing and 165 and 205 kDa under reducing conditions is recognized by immunoprecipitation and Western blot analysis. Staphylococcus aureus V8 protease maps of these two proteins show many shared bands. Crossed immunoprecipitation using BRN-1 and 7E9, a previously described mAb reported to identify the 190-kDa mouse CR1 and a smaller 150-kDa protein, indicates that both antibodies react with the same proteins. Therefore, by using BRN-1 we have now linked the genetic mouse **CR2** to its functional, biochemically characterized gene product. The observation that BRN-1 also recognizes a second 190-kDa mouse protein defined functionally as a homologue of human CR1, and that these proteins have very similar peptide maps, provides strong evidence that these two proteins are expressed by a single mouse **CR2**/CR1 transcription unit.
CT Check Tags: Animal; Comparative Study; Support, Non-U.S. Gov't
Amino Acid Sequence
Antigens, Differentiation, B-Lymphocyte: CH, chemistry
Antigens, Differentiation, B-Lymphocyte: GE, genetics
Antigens, Differentiation, B-Lymphocyte: IM, immunology
Base Sequence
Blotting, Northern
Cloning, Molecular
DNA: GE, genetics
Genes, Structural
Mice
Molecular Sequence Data
Peptide Mapping
Precipitin Tests
Receptors, Complement: CH, chemistry
***Receptors, Complement: GE, genetics**
Receptors, Complement: IM, immunology
Receptors, Complement 3b
Receptors, Complement 3d
Recombinant Fusion Proteins: GE, genetics
Recombinant Fusion Proteins: IM, immunology
Recombinant Fusion Proteins: IP, isolation & purification
Restriction Mapping
RN 9007-49-2 (DNA)
CN 3 (Antigens, Differentiation, B-Lymphocyte); 3 (Receptors, Complement); 3 (Receptors, Complement 3b); 3 (Receptors, Complement 3d); 3 (Recombinant Fusion Proteins)

L[illegible] ANSWER [illegible] OF [illegible] MEDLINE
AN **90324211** MEDLINE

AN 90324211 PubMed ID: 1695627
TI Structural requirements for C3d,g Epstein-Barr virus receptor **CR2** (CD21), ligand binding, internalization, and viral infection.
AU Carel J C; Myones B L; Frazier B; **Holers V M**
CS Howard Hughes Medical Institute Laboratories, Washington University School of Medicine, St. Louis, Missouri 63110.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1990 Jul 15) 265 (20) 11294-9.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199008
ED Entered STN: 19900813
Last Updated on STN: 19960129
Entered Medline: 19900830
AB The structure of **CR2**, the human C3d,g/EBV receptor (**CR2** /CD21) consists of 15 or 16 60-70 amino acid repeats called short consensus repeats (SCRs) followed by a transmembrane and a 34-amino acid intracytoplasmic domain. Functions of **CR2** include binding the human complement component C3d,g when it is covalently attached to targets or cross-linked in the fluid phase. In addition, **CR2** binds the Epstein-Barr virus (EBV) and mediates internalization of EBV and subsequent infection of cells. In order to explore functional roles of the repetitive extracytoplasmic SCR structure and the intracytoplasmic domain of **CR2**, we have created truncated **CR2** (rCR2) mutants bearing serial deletions of extracytoplasmic SCRs and also the intracytoplasmic tail. We then stably transfected these rCR2 mutants into two cell lines, murine fibroblast L cells and human erythroleukemic K562 cells. Phenotypic analysis of these expressed mutants revealed that 1) The C3d,g- and EBV-binding sites are found in the two amino-terminal SCRs of **CR2**, 2) expression of SCRs 3 and 4 is further required for high affinity binding to soluble cross-linked C3d,g, 3) the intracytoplasmic domain of **CR2** is not required for binding C3d,g or EBV but is necessary for internalization of cross-linked C3d,g as well as for EBV infection of cells, 4) monoclonal anti-**CR2** antibodies with similar activities react with single widely separated epitopes, and 5) no functional roles can yet be clearly assigned to SCRs 5-15, as rCR2 mutants not containing these SCRs show no major differences from wild-type rCR2 in binding or internalizing cross-linked C3d,g or mediating EBV binding and infection.
CT Check Tags: Animal; Human; Support, Non-U.S. Gov't
Antibodies, Monoclonal
Antigens, Differentiation, B-Lymphocyte: GE, genetics
Antigens, Differentiation, B-Lymphocyte: ME, metabolism
Base Sequence
Cell Line
*Complement 3: ME, metabolism
*Complement 3d: ME, metabolism
DNA Mutational Analysis
Endocytosis
Epitopes
*Herpesvirus 4, Human: ME, metabolism
Mice
Molecular Sequence Data
Oligonucleotides
Receptors, Complement: GE, genetics
***Receptors, Complement: ME, metabolism**
Receptors, Complement 3d
*Receptors, Virus: ME, metabolism
Structure-Activity Relationship
Tumor Virus Infections: ME, physiopathology
RN 80248-48-0 (Complement 3d)

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IN    1  Antibodies, Monoclonal ; 1  Antigens, Differentiation, B-Lymphocyte ;
      Complement 3 ; 1  Epitopes ; 1  Oligonucleotides ; 1  Receptors,
      Complement ; 1  Receptors, Complement 3d ; 1  Receptors, Virus ; 1
      Complement 3g

=> d his

     (FILE 'HOME' ENTERED AT 10:40:04 ON 09 NOV 2002)
               SET COST OFF

     FILE 'BIOSIS' ENTERED AT 10:41:12 ON 09 NOV 2002
               E HOLERS V/AU
L1          231 S E5-E6
               E CHEN X/AU
L2         1046 S E1,E19
L3           5  S E150
L4           4  S E45-E48
L5         1384 S L1-L4
L6          161 S COMPLEMENT RECEPTOR (L) TYPE 2
L7         1017 S CR2
L8          136 S COMPLEMENT RECEPTOR 2
L9            4 S COMPLEMENT RECEPTOR (L) TYPE TWO
L10          17 S COMPLEMENT RECEPTOR (L) TYPE II
L11          69 S L5 AND L6-L10
L12          11 S L11 AND STRUCTUR?
L13           1 S L11 AND CONFORMATION?
L14           1 S L11 AND X RAY
L15          14 S L11 AND (3D OR 3 OR THREE)(W)(D OR DIMENSION?) OR AXIS OR AXI
L16           1 S L11 AND COMBINATOR?
L17          46 S L11 AND (CRYSTAL? OR XRAY? OR DIFFRACT? OR COORDINAT?)
L18           0 S L11 AND 1?530 CC
L19           0 S L11 AND 04500 CC
L20          52 S L12-L17
L21          14 S L20 NOT AB/BA
               SEL DN AN 6 16 14 26
L22           4 S L11 AND E1-E8
L23          20 S L20 NOT L21
               SEL DN AN 13
L24           1 S L23 AND E4-E11
               SEL DN 4 L25
L25           1 S L23 AND E11
L26           6 S L21,L24,L25
L27          50 S L19 NOT L26
               SEL DN AN 41 50 L27
L28           1 S E12-E15
L29           4 S L26,L24 AND L1-L28

     FILE 'BIOSIS' ENTERED AT 11:01:14 ON 09 NOV 2002

     FILE 'HCAPLUS' ENTERED AT 11:01:35 ON 09 NOV 2002
               E HOLERS V/AU
L30          13 S E4,E5
               E CHEN X/AU
L31         771 S E7,E13
               E CHEN XIAO/AU
L32         144 S E3,E5
L33          13 S E167,E169
L34        8882 S L5-L10
               E COMPLEMENT RECEPTOR/CT
L35         328 S E14
               E E7+ALL
L36        1884 S E19
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L57          2154 S E4
L58           108 S E10
L59            65 S L55-L58 AND L34-L36
L61             4 S L59 AND (STRUCTURE OR "STRUCTURES")/CW
                E MOLECULAR STRUCTURE/CT
L62        948752 S E3+NT OR E11+NT OR E21+NT OR E5 +NT OR E24+NT
                E E3+ALL
L63            15 S (E224+NT OR E228+NT OR E229+NT OR E230+NT) AND L34-L36
L64           869 S (E225+NT OR E230+NT OR E231+NT) AND L34-L36
L65            73 S (E236+NT OR E241+NT) AND L34-L36
L66           916 S L62-L64
L67           961 S (MOLECULAR? OR CRYSTAL? OR 3D OR 3 OR THREE OR THIRD(W)D OR
L68            25 S (NONPLANAR? OR NON PLANAR? OR AUTOMAT? OR SEMIAUTOMAT? OR AUT
L69           266 S L66,L67 AND L34
L70            15 S L68 AND STRUCTUR?/CW
L80            14 S L69 AND MOLECUL?/CW
                SEL DN AN 3 6 8 L50
L51             3 S L50 AND E1-E9
                E CONFORMATION/CT
                E E3+ALL
L52        174400 S E3,E2+NT
L53        504981 S E84+NT
                E MOLECULAR MODEL/CT
                E E4+ALL
L54       1090719 S E1 OR E2+NT OR E9+NT OR E10+NT
                E MOLECULAR/CT
                E E8+ABB
                E E3+ALL
L55         79754 S E1+NT OR E22+NT OR E32+NT
                E SECONDARY STRUCTURE/CT
                E E3+ABB
                E E3+ALL
L56         22803 S E4,E3+NT
L57        299576 S E1,E2
L58           294 S L55-L58 AND L52-L57
L59            74 S L54 AND L58
L60             7 S L59 AND STRUCTUR?/TI
L61             9 S L51,L60
L62            10 S L40,L61
L63            10 S L62 AND L30-L62

     FILE 'HCAPLUS' ENTERED AT 11:24:56 ON 09 NOV 2002

     FILE 'MEDLINE' ENTERED AT 11:25:07 ON 09 NOV 2002
L64           114 S L6
L65            68 S L8
L66             9 S L9
L67            13 S L10
L68           764 S L7
L69           114 S L61-L67 AND L58
L70           105 S L64-L67,L69
L71           620 S L68 NOT L70
                E RECEPTORS, COMPLEMENT/CT
                E E21+ALL
L72           647 S E17+NT
                E RECEPTORS, COMPLEMENT/CT
                E E3+ALL
L73          6391 S E13+NT
L74           165 S L70 AND L72-L73
L75            30 S L70 NOT L74
                SEL DN AN 3 4
L76             2 S E1-E5 AND L75
L77           167 S L74,L76
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L74          6393 S L71,L73,L77
                  E HOLBERG V/AU
L75           111 S E4,E8
                  E CHEN X/AU
L80          1556 S E3,E11
L81             4 S E82
L82            76 S L64-L74 AND L79-L81
                  SEL DN AN 11 15 16 02-04
L83             6 S E1-E16 AND L82
                  E MODELS, MOLECULAR/CT
                  E E1+ALL
L84        363250 S E4+NT
                  E CRYSTAL/CT
                  E E82+ALL
L85         35974 S E11+NT
L86           189 S L64,L85 AND L64-L78
L87             3 S L86 AND L83
L88             6 S L83,L87
L89           186 S L86 NOT L88
L90           181 S L89 NOT AB
L91             5 S L89 NOT L90
                  SEL L90 DN AN 1  102 137
L92             3 S L90 AND E1-E9
L93             9 S L88,L91 AND L64-L92

      FILE 'MEDLINE' ENTERED AT 11:39:04 ON 09 NOV 2002
                  E J INFO JT
                  E JOU/JT
                  E JOURNAL I/JT
                  E JOURNAL OF INF/JT

      FILE 'HCAPLUS' ENTERED AT 11:40:01 ON 09 NOV 2002
                  E J INFO JT
                  E JOU INFO/JT
                  E JOURN INFO/JT
                  E JOURNAL INFO/JT
                  E JOURNAL OF INFO/JT

      FILE 'WPIX' ENTERED AT 11:41:31 ON 09 NOV 2002
L94             6 S L7 OR L8 OR L9 OR L10
                  E HOLBERG V/AU
                  E CHEN X/AU
L95             4 S E3-E15 AND (COMPLEMENT OR CR2)
```